

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/572,195
Source: IFWP
Date Processed by STIC: 4/6/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/06/2006

PATENT APPLICATION: US/10/572,195

TIME: 10:54:17

Input Set : A:\PCT - Sequence listing for submission.txt1.TXT

Output Set: N:\CRF4\04062006\J572195.raw

3 <110> APPLICANT: PERFORMANCE GENOMICS, INC.
 5 <120> TITLE OF INVENTION: Insulin-Like Growth Factor-1 Receptor (IGF-1R) Polymorphic
 6 Alleles and Use of the Same to Identify DNA Markers for
 7 Reproductive Longevity
 9 <130> FILE REFERENCE: 31649-2137
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/572,195
 C--> 12 <141> CURRENT FILING DATE: 2006-03-15
 12 <150> PRIOR APPLICATION NUMBER: US 10/662,613
 13 <151> PRIOR FILING DATE: 2003-09-15
 16 <160> NUMBER OF SEQ ID NOS: 22
 18 <170> SOFTWARE: PatentIn version 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4500
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Mus musculus
 25 <400> SEQUENCE: 1

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 28 gccgcgctct ctctctggcc gacgagtggg gaaatctgtg ggcccggcat tgacatccgc 120
 30 aacgactatc agcagctgaa gcgcctggaa aactgcacgg tgatcgaggg ctctctccac 180
 32 atcctgctca tctccaaggc cgaggactac cgaagctacc gcttccccaa gctcaccgtc 240
 34 atcaactgagt acttgctgct ctcccgagtc gctggcctcg agagcctggg agacctcttc 300
 36 cccaacctca cagtcattccg ttggtggaaa ctctcttaca actacgcact ggtcatcttc 360
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 40 atcaggattg agaagaacgc cgacctctgt tacctctcca ccatagactg gtctctcatc 480
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 50 acaccggacg acaacacaac ctgcgtggcc tgcagacact actactaaa aggcgtgtgt 780
 52 gtgcctgctt gccgcctgg cactacagg ttccagggtt ggcgctgtgt ggatcgcgat 840
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84 tatgtcaagg ctgtgacct caccatggtg gaaaacgacc atatccgtgg ggccaaaagt 1800
86 gaaatcttgt acattcgcac caatgcttca gtcccttcca tccccctaga tgtcctctca 1860
88 gcatcaaact cttcctctca gctgattgtg aagtggaaac ctccaactct gcccaatggt 1920
90 aacttgagtt actacattgt gaggtggcag cggcagcccc aggatggtta cctgtaccgg 1980
92 cacaactact gctccaaaga caaaataccc atcagaaagt acgccgatgg taccatcgac 2040
94 gtggaggagg tgacggaaaa tccaagaca gaagtgtgtg gtggtgataa agggccatgc 2100
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98 aaagtctttg agaatttctt tcacaattcc atctttgtgc ccaggccccga aaggaggcgg 2220
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126 accatgaacc gggagctcgg acaagggtcc tttgggatgg tctatgaagg agtggccaag 3060
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130 agtatgcgtg aaagaatcga gtttctcaac gaggcctcgg tgatgaagga gttcaattgt 3180
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138 attgcagatg gcattggccta cctcaatgcc aacaagttcg tccacagaga ccttgctgct 3420
140 aggaactgca tggtagccga agatttcaca gtcaaaattg gagatttcgg tatgacacga 3480
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152 ttcttgagga tcatcggcag catcaaggat gagatggagc ccagcttcca ggaggtctcc 3840
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166 caggttgtaa caatctattc acaagcctcc tgtacctcag tggatcttca gacctgccat 4260
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177 <210> SEQ ID NO: 2

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178 <211> LENGTH: 1373

179 <212> TYPE: PRT

180 <213> ORGANISM: Mus musculus

182 <400> SEQUENCE: 2

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189 20 25 30
192 Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Tyr Gln Gln Leu Lys Arg
193 35 40 45
196 Leu Glu Asn Cys Thr Val Ile Glu Gly Phe Leu His Ile Leu Leu Ile
197 50 55 60
200 Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
201 65 70 75 80
204 Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
205 85 90 95
208 Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
209 100 105 110
212 Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
213 115 120 125
216 Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
217 130 135 140
220 Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Ile Asp Trp Ser Leu Ile
221 145 150 155 160
224 Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
225 165 170 175
228 Glu Cys Gly Asp Leu Cys Pro Gly Thr Leu Glu Glu Lys Pro Met Cys
229 180 185 190
232 Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr
233 195 200 205
236 Asn Arg Cys Gln Lys Met Cys Pro Ser Val Cys Gly Lys Arg Ala Cys
237 210 215 220
240 Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys His
241 225 230 235 240
244 Thr Pro Asp Asp Asn Thr Thr Cys Val Ala Cys Arg His Tyr Tyr Tyr
245 245 250 255
248 Lys Gly Val Cys Val Pro Ala Cys Pro Pro Gly Thr Tyr Arg Phe Glu
249 260 265 270
252 Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Pro Asn Ala
253 275 280 285
256 Glu Ser Ser Asp Ser Asp Gly Phe Val Ile His Asp Asp Glu Cys Met
257 290 295 300
260 Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Ser Thr Gln Ser Met Tyr
261 305 310 315 320
264 Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Gly Asp Glu Glu
265 325 330 335
268 Lys Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln
269 340 345 350
272 Gly Cys Thr Ile Leu Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly

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273          355          360          365
276 Asn Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val
277          370          375          380
280 Val Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu
281 385          390          395          400
284 Ser Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu
285          405          410          415
288 Gly Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu
289          420          425          430
292 Trp Asp Trp Asn His Arg Asn Leu Thr Val Arg Ser Gly Lys Met Tyr
293          435          440          445
296 Phe Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu
297          450          455          460
300 Glu Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr
301 465          470          475          480
304 Arg Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu Arg Phe
305          485          490          495
308 Thr Ser Thr Thr Thr Trp Lys Asn Arg Ile Ile Ile Thr Trp His Arg
309          500          505          510
312 Tyr Arg Pro Pro Asp Tyr Arg Asp Leu Ile Ser Phe Thr Val Tyr Tyr
313          515          520          525
316 Lys Glu Ala Pro Phe Lys Asn Val Thr Glu Tyr Asp Gly Gln Asp Ala
317          530          535          540
320 Cys Gly Ser Asn Ser Trp Asn Met Val Asp Val Asp Leu Pro Pro Asn
321 545          550          555          560
324 Lys Glu Gly Glu Pro Gly Ile Leu Leu His Gly Leu Lys Pro Trp Thr
325          565          570          575
328 Gln Tyr Ala Val Tyr Val Lys Ala Val Thr Leu Thr Met Val Glu Asn
329          580          585          590
332 Asp His Ile Arg Gly Ala Lys Ser Glu Ile Leu Tyr Ile Arg Thr Asn
333          595          600          605
336 Ala Ser Val Pro Ser Ile Pro Leu Asp Val Leu Ser Ala Ser Asn Ser
337          610          615          620
340 Ser Ser Gln Leu Ile Val Lys Trp Asn Pro Pro Thr Leu Pro Asn Gly
341 625          630          635          640
344 Asn Leu Ser Tyr Tyr Ile Val Arg Trp Gln Arg Gln Pro Gln Asp Gly
345          645          650          655
348 Tyr Leu Tyr Arg His Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg
349          660          665          670
352 Lys Tyr Ala Asp Gly Thr Ile Asp Val Glu Glu Val Thr Glu Asn Pro
353          675          680          685
356 Lys Thr Glu Val Cys Gly Gly Asp Lys Gly Pro Cys Cys Ala Cys Pro
357          690          695          700
360 Lys Thr Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg
361 705          710          715          720
364 Lys Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro
365          725          730          735
368 Glu Arg Arg Arg Arg Asp Val Met Gln Val Ala Asn Thr Thr Met Ser
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372 Ser Arg Ser Arg Asn Thr Thr Val Ala Asp Thr Tyr Asn Ile Thr Asp
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376 Pro Glu Glu Phe Glu Thr Glu Tyr Pro Phe Phe Glu Ser Arg Val Asp
377      770      775      780
380 Asn Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr
381 785      790      795      800
384 Arg Ile Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys
385      805      810      815
388 Ser Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly Ala
389      820      825      830
392 Asp Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser
393      835      840      845
396 Ile Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu
397      850      855      860
400 Met Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys
401 865      870      875      880
404 Val Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg
405      885      890      895
408 Leu Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser
409      900      905      910
412 Gly Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Pro Ala Lys
413      915      920      925
416 Thr Thr Tyr Glu Asn Phe Met His Leu Ile Ile Ala Leu Pro Val Ala
417      930      935      940
420 Ile Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His
421 945      950      955      960
424 Arg Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser
425      965      970      975
428 Val Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu
429      980      985      990
432 Trp Glu Val Ala Arg Glu Lys Ile Thr Met Asn Arg Glu Leu Gly Gln
433      995      1000      1005
436 Gly Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val
437      1010      1015      1020
440 Lys Asp Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu
441      1025      1030      1035
444 Ala Ala Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser
445      1040      1045      1050
448 Val Met Lys Glu Phe Asn Cys His His Val Val Arg Leu Leu Gly
449      1055      1060      1065
452 Val Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu Leu Met
453      1070      1075      1080
456 Thr Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu
457      1085      1090      1095
460 Val Glu Gln Asn Asn Leu Val Leu Ile Pro Pro Ser Leu Ser Lys
461      1100      1105      1110
464 Met Ile Gln Met Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr Leu
465      1115      1120      1125
468 Asn Ala Asn Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 3177,3178

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:6716 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:3120